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RAW SEQUENCE LISTING   DATE: 01/11/2001
PATENT APPLICATION: US/09/746,390   TIME: 16:55:59

Input Set : A:\Gfb5.app
Output Set: N:\CRF3\01112001\I746390.raw

ENTERED

SEQUENCE LISTING
3 (1) GENERAL INFORMATION:
5   (i) APPLICANT: Jens Kossmann
6   Ruth Lorberth
8   (ii) TITLE OF INVENTION: PLANTS WHICH SYNTHESIZE A MODIFIED STARCH,
9   PROCESS FOR THE PRODUCTION THEREOF AND MODIFIED STARCH
12   (iii) NUMBER OF SEQUENCES: 4
14   (iv) CORRESPONDENCE ADDRESS:
15   (A) ADDRESSEE: FISH & NEAVE
16   (B) STREET: 1251 Avenue of the Americas
17   (C) CITY: New York
18   (D) STATE: New York
19   (E) COUNTRY: USA
20   (F) ZIP: 10020
22   (v) COMPUTER READABLE FORM:
23   (A) MEDIUM TYPE: Floppy disk
24   (B) COMPUTER: IBM PC compatible
25   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
28   (vi) CURRENT APPLICATION DATA:
C--> 29   (A) APPLICATION NUMBER: US/09/746,390
C--> 30   (B) FILING DATE: 21-Dec-2000
C--> 31   (C) CLASSIFICATION:
41   (vii) PRIOR APPLICATION DATA:
34   (A) APPLICATION NUMBER: PCT/EP96/04109
35   (B) FILING DATE: 19-SEP-1996
38   (A) APPLICATION NUMBER: DE 19547733.2
39   (B) FILING DATE: 20-DEC-1995
42   (A) APPLICATION NUMBER: DE 19534759.5
43   (B) FILING DATE: 19-SEP-1995
45   (viii) ATTORNEY/AGENT INFORMATION:
46   (A) NAME: Haley Jr., James F.
47   (B) REGISTRATION NUMBER: 27,794
48   (C) REFERENCE/DOCKET NUMBER: GFB-5
50   (ix) TELECOMMUNICATION INFORMATION:
51   (A) TELEPHONE: 212-596-9000
52   (B) TELEFAX: 212-596-9090
54 (2) INFORMATION FOR SEQ ID NO: 1:
56   (i) SEQUENCE CHARACTERISTICS:
57   (A) LENGTH: 4856 base pairs
58   (B) TYPE: nucleotide
59   (C) STRANDEDNESS: single
60   (D) TOPOLOGY: linear
62   (ii) MOLECULE TYPE: cDNA to mRNA
64   (vi) ORIGINAL SOURCE:
65   (A) ORGANISM: Solanum tuberosum
66   (B) STRAIN: C.V. Berolina

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Output Set: N:\CRF3\01112001\I746390.raw

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68      (ix) FEATURE:
69          (A) NAME/KEY: CDS
70          (B) LOCATION:105..4497
73      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
75  CATCTTCATC GAATTCTCG AAGCTTCTTC GCTAATTTCC TGGTTTCTTC ACTCAAAATC          60
77  GACGTTTCTA GCTCAACTTG AGTGAATTAA GCCACTGGGA GGAT ATG AGT AAT TCC         116
78                                                   Met Ser Asn Ser
79                                                    1
81  TTA GGG AAT AAC TTG CTG TAC CAG GGA TTC CTA ACC TCA ACA GTG TTG         164
82  Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr Ser Thr Val Leu
83   5                  10                  15                  20
85  GAA CAT AAA AGT AGA ATC AGT CCT CCT TGT GTT GGA GGC AAT TCT TTG         212
86  Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu
87                  25                  30                  35
88  TTT CAA CAA CAA GTG ATC TCG AAA TCA CCT TTA TCA ACT GAG TTT CGA         260
89  Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser Thr Glu Phe Arg
90              40                  45                  50
92  GGT AAC AGG TTA AAG GTG CAG AAA AAG AAA ATA CCT ATG GAA AAG AAG         308
93  Gly Asn Arg Leu Lys Val Gln Lys Lys Lys Ile Pro Met Glu Lys Lys
94          55                  60                  65
96  CGT GCT TTT TCT AGT TCT CCT CAT GCT GTA CTT ACC ACT GAT ACC TCT         356
97  Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr Thr Asp Thr Ser
98      70                  75                  80
100 TCT GAG CTA GCA GAA AAG TTC AGT CTA GGG GGG AAT ATT GAG CTA CAG         404
101 Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn Ile Glu Leu Gln
102 85                  90                  95                 100
104 GTT GAT GTT AGG CCT CCC ACT TCA GGT GAT GTG TCC TTT GTG GAT TTT         452
105 Val Asp Val Arg Pro Pro Thr Ser Gly Asp Val Ser Phe Val Asp Phe
106                 105                 110                 115
108 CAA GTA ACA AAT GGT AGT GAT AAA CTG TTT TTG CAC TGG GGG GCA GTA         500
109 Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His Trp Gly Ala Val
110                 120                 125                 130
112 AAA TTC GGG AAA GAA ACA TGG TCT CTT CCG AAT GAT CGT CCA GAT GGG         548
113 Lys Phe Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp Arg Pro Asp Gly
114         135                 140                 145
116 ACC AAA GTG TAC AAG AAC AAA GCA CTT AGA ACT CCA TTT GTT AAA TCT         596
117 Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro Phe Val Lys Ser
118     150                 155                 160
120 GGC TCT AAC TCC ATC CTG AGA CTG GAG ATA CGA GAC ACT GCT ATC GAA         644
121 Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp Thr Ala Ile Glu
122 165                 170                 175                 180
124 GCT ATT GAG TTT CTC ATA TAC GAT GAA GCC CAC GAT AAA TGG ATA AAG         692
125 Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp Lys Trp Ile Lys
126                 185                 190                 195
128 AAT AAT GGT GGT AAT TTT CGT GTC AAA TTG TCA AGA AAA GAG ATA CGA         740
129 Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg Lys Glu Ile Arg
130                 200                 205                 210
132 GGC CCA GAT GTT TCT GTT CCT GAG GAG CTT GTA CAG ATC CAA TCA TAT         788
133 Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln Ile Gln Ser Tyr
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134        215                  220                 225
137 TTG AGG TGG GAG AGG AAG GCA AAA CAG AAT TAC CCC CCT GAG AAA GAG      836
138 Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro Pro Glu Lys Glu
139     230                235                 240
141 AAG GAG GAA TAT GAG GCT GCT CGA ACT GTG CTA CAG GAG GAA ATA GCT      884
112 Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln Glu Glu Ile Ala
143 245                250                 255                 260
145 CGT GGT GCT TCC ATA CAG GAC ATT CGA GCA AGG CTA ACA AAA ACT AAT      932
146 Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu Thr Lys Thr Asn
147                265                 270                 275
148 GAT AAA AGT CAA AGC AAA GAA GAG CCT CTT CAT GTA ACA AAG AGT GAT      980
149 Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val Thr Lys Ser Asp
150                280                 285                 290
152 ATA CCT GAT GAC CTT GCC CAA GCA CAA GCT TAC ATT AGG TGG GAG AAA      1028
153 Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile Arg Trp Glu Lys
154        295                 300                 305
156 GCA GGA AAG CCG AAC TAT CCT CCA GAA AAG CAA ATT GAA GAA CTC GAA      1076
157 Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile Glu Glu Leu Glu
158     310                315                 320
160 GAA GCA AGA AGA GAA TTG CAA CTT GAG CTT GAG AAA GGC ATT ACC CTT      1124
161 Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys Gly Ile Thr Leu
162 325                330                 335                 340
164 GAT GAG TTG CGG AAA ACG ATT ACA AAA GGG GAG ATA AAA ACT AAG GTG      1172
165 Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile Lys Thr Lys Val
166        345                 350                 355
168 GAA AAG CAC CTG AAA AGA AGT TCT TTT GCC GTT GAA AGA ATC CAA AGA      1220
169 Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu Arg Ile Gln Arg
170        360                 365                 370
172 AAG AAG AGA GAC TTT GGG CAT CTT ATT AAT AAG TAT ACT TCC AGT CCT      1268
173 Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr Thr Ser Ser Pro
174        375                 380                 385
176 GCA GTA CAA GTA CAA AAG GTC TTG GAA GAA CCA CCA GCC TTA TCT AAA      1316
177 Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro Ala Leu Ser Lys
178     390                395                 400
180 ATT AAG CTG TAT GCC AAG GAG AAG GAG GAG CAG ATT GAT GAT CCG ATC      1364
181 Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile Asp Asp Pro Ile
182 405                410                 415                 420
184 CTA AAT AAA AAG ATC TTT AAG GTC GAT GAT GGG GAG CTA CTG GTA CTG      1412
185 Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu Leu Leu Val Leu
186                425                 430                 435
188 GTA GCA AAG TCC TCT GGG AAG ACA AAA GTA CAT CTA GCT ACA GAT CTG      1460
189 Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu Ala Thr Asp Leu
190        440                 445                 450
192 AAT CAG CCA ATT ACT CTT CAC TGG GCA TTA TCC AAA AGT CCT GGA GAG      1508
193 Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys Ser Pro Gly Glu
194        455                 460                 465
196 TGG ATG GTA CCA CCT TCA AGC ATA TTG CCT CCT GGG TCA ATT ATT TTA      1556
197 Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly Ser Ile Ile Leu
198     470                475                 480
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200 GAC AAG GCT GCC GAA ACA CCT TTT TCA GCC AGT TCT TCT GAT GGT CTA        1604
201 Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser Asp Gly Leu
202 485                     490                 495                 500
204 ACT TCT AAG GTA CAA TCT TTG GAT ATA GTA ATT GAA GAT GGC AAT TTT        1652
205 Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu Asp Gly Asn Phe
206                         505                 510                 515
208 GTG GGG ATG CCA TTT GTT CTT TTG TCT GGT GAA AAA TGG ATT AAG AAC        1700
209 Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys Trp Ile Lys Asn
210                         520                 525                 530
212 CAA GGG TCG GAT TTC TAT GTT GGC TTC AGT GCT GCA TCC AAA TTA GCA        1748
213 Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala Ser Lys Leu Ala
214                         535                 540                 545
216 CTC AAG GCT GCT GGG GAT GGC AGT GGA ACT GCA AAG TCT TTA CTG GAT        1796
217 Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys Ser Leu Leu Asp
218     550                     555                 560
220 AAA ATA GCA GAT ATG GAA AGT GAG GCT CAG AAG TCA TTT ATG CAC CGG        1844
221 Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser Phe Met His Arg
222 565                     570                 575                 580
224 TTT AAT ATT GCA GCT GAC TTG ATA GAA GAT GCC ACT AGT GCT GGT GAA        1892
225 Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr Ser Ala Gly Glu
226                         585                 590                 595
228 CTT GGT TTT GCT GGA ATT CTT GTA TGG ATG AGG TTC ATG GCT ACA AGG        1940
229 Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe Met Ala Thr Arg
230                         600                 605                 610
232 CAA CTG ATA TGG AAC AAA AAC TAT AAC GTA AAA CCA CGT GAA ATA AGC        1988
233 Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu Ile Ser
234     615                     620                 625
236 AAG GCT CAG GAC AGA CTT ACA GAC TTG TTG CAG AAT GCT TTC ACC AGT        2036
237 Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn Ala Phe Thr Ser
238     630                     635                 640
240 CAC CCT CAG TAC CGT GAA ATT TTG CGG ATG ATT ATG TCA ACT GTT GGA        2084
241 His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Gly
242 645                     650                 655                 660
245 CGT GGA GGT GAA GGG GAT GTA GGA CAG CGA ATT AGG GAT GAA ATT TTG        2132
246 Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu Ile Leu
247                         665                 670                 675
249 GTC ATC CAG AGG AAC AAT GAC TGC AAG GGT GGT ATG ATG CAA GAA TGG        2180
250 Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met Met Gln Glu Trp
251                         680                 685                 690
253 CAT CAG AAA TTG CAT AAT AAT ACT AGT CCT GAT GAT GTT GTG ATC TGT        2228
254 His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys
255     695                     700                 705
257 CAG GCA TTA ATT GAC TAC ATC AAG AGT GAT TTT GAT CTT GGT GTT TAT        2276
258 Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr
259     710                     715                 720
261 TGG AAA ACC CTG AAT GAG AAC GGA ATA ACA AAA GAG CGT CTT TTG AGT        2324
262 Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu Arg Leu Leu Ser
263 725                     730                 735                 740
265 TAT GAC CGT GCT ATC CAT TCT GAA CCA AAT TTT AGA GGA GAT CAA AAG        2372
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266  Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys
267                  745             750                 755
268  GGT GGT CTT TTG CGT GAT TTA GGT CAC TAT ATG AGA ACA TTG AAG GCA          2420
269  Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg Thr Leu Lys Ala
270              760             765                 770
272  GTT CAT TCA GGT CCA GAT CTT GAG TCT GCT ATT GCA AAC TGC ATG GGC          2468
273  Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Asn Cys Met Gly
274          775             780             785
276  TAC AAA ACT GAG GGA GAA GGC TTT ATG GTT GGA GTC CAG ATA AAT CCT          2516
277  Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile Asn Pro
278      790             795             800
280  GTA TCA GGC TTG CCA TCT GGC TTT CAG GAC CTC CTC CAT TTT GTC TTA          2564
281  Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu His Phe Val Leu
282  805             810             815                 820
284  GAC CAT GTG GAA GAT AAA AAT GTG GAA ACT CTT CTT GAG AGA TTG CTA          2612
285  Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu Glu Arg Leu Leu
286              825             830             835
288  GAG GCT CGT GAG GAG CTT AGG CCC TTG CTT CTC AAA CCA AAC AAC CGT          2660
289  Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys Pro Asn Asn Arg
290              840             845             850
292  CTA AAG GAT CTG CTG TTT TTG GAC ATA GCA CTT GAT TCT ACA GTT AGA          2708
293  Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp Ser Thr Val Arg
294          855             860             865
296  ACA GCA GTA GAA AGG GGA TAT GAA GAA TTG AAC AAC GCT AAT CCT GAG          2756
297  Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn Ala Asn Pro Glu
298      870             875             880
300  AAA ATC ATG TAC TTC ATC TCC CTC GTT CTT GAA AAT CTC GCA CTC TCT          2804
301  Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser
302  885             890             895                 900
304  GTG GAC GAT AAT GAA GAT CTT GTT TAT TGC TTG AAG GGA TGG AAT CAA          2852
305  Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys Gly Trp Asn Gln
306              905             910             915
308  GCT CTT TCA ATG TCC AAT GGT GGG GAC AAC CAT TGG GCT TTA TTT GCA          2900
309  Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp Ala Leu Phe Ala
310              920             925             930
312  AAA GCT GTG CTT GAC AGA ACC CGT CTT GCA CTT GCA AGC AAG GCA GAG          2948
313  Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala Ser Lys Ala Glu
314          935             940             945
316  TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA TCA ATA          2996
317  Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly Ser Ile
318      950             955             960
320  CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA ATT ATA          3044
321  Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu Ile Ile
322  965             970             975                 980
324  CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA CTC GAT          3092
325  Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg Leu Asp
326              985             990             995
328  CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT ATC AGT          3140
329  Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/746,390

DATE: 01/11/2001
TIME: 16:56:00

Input Set : A:\Gfb5.app
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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:31 M:220 C: Keyword misspelled or invalid format, [(C) CLASSIFICATION:]
L:415 M:361 W: Invalid Split Codon, Sequence data for SEO ID#: 1
L:897 M:361 W: Invalid Split Codon, Sequence data for SEO ID#: 3